



#4

SEQUENCE LISTING

<110> Cyclacel

<120> Compositions and Methods for Monitoring the Modification of Modification  
Dependent Binding Partner Polypeptides

<130> 10069/1062

<140> 09/770102

<141> 2001-01-25

<150> US 60/179283

<151> 2000-01-31

<160> 57

<170> PatentIn version 3.0

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<211> 17

<212> PRT

<213> Unknown

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<223> ADP-ribosylation domain

<220>

<221> DOMAIN

<222> (1)..(17)

<223> ADT-ribosylation site

<400> 1

Met Leu Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Asp  
1 5 10 15

Asp

<210> 2

<211> 10

<212> PRT

<213> Unknown

<220>

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<222> (1)..(10)

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Phe Lys Gln Arg Gln Thr Arg Gln Phe Lys  
 1 5 10

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 <222> (1)..(30)  
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<400> 3

Met Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro  
 1 5 10 15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His  
 20 25 30

<210> 4  
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<400> 4

His Gly Ser Gly Ala Trp Leu Leu Pro Val Ser Leu Val Lys Arg Lys  
 1 5 10 15

Thr Thr Leu Ala Pro  
 20

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Gly Thr Thr Ser Thr Ile Gln Thr Ala Pro  
1 5 10

<210> 6  
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<400> 6

Ser Ala Val Ser Ser Ala Asp Gly Thr Val Leu Lys  
1 5 10

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<400> 7

Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr  
1 5 10 15

Leu Pro

<210> 8  
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<400> 8

Met Ala Gly Gly Pro Ala Asp Thr Ser Asp Pro Leu  
1 5 10

<210> 9  
<211> 13  
<212> PRT  
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<400> 9

Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr  
1 5 10

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<220>  
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<222> (1)..(8)  
<223> X at position 3 may be any amino acid

<400> 10

Arg Arg Xaa Arg Arg Xaa Ser Thr  
1 5

<210> 11  
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<400> 11

Lys Xaa Xaa Ser Xaa  
1 5

<210> 12  
<211> 3  
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<222> (1)..(3)  
<223> Consensus sequence, Xaa is any amino acid

<400> 12

Arg Xaa Thr  
1

<210> 13  
<211> 5  
<212> PRT  
<213> Unknown

<220>  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 13

Arg Xaa Xaa Ser Xaa  
1 5

<210> 14  
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<212> PRT  
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<220>  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 14

Xaa Ser Arg Xaa  
1

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<211> 8  
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<213> Unknown

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<223> Consensus sequence, each Xaa is any amino acid

<400> 15

Xaa Arg Xaa Xaa Ser Xaa Arg Xaa  
1 5

<210> 16  
<211> 6  
<212> PRT  
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<220>  
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<400> 16

Xaa Arg Xaa Xaa Ser Xaa  
1 5

<210> 17  
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<220>  
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<223> Consensus sequence

<400> 17

Ser Glu Leu Ser Arg Arg  
1 5

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<212> PRT  
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<220>  
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<400> 18

Xaa Ser Xaa Xaa Ser Xaa  
1 5

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<400> 19

Xaa Ser Xaa Glu Xaa  
1 5

<210> 20  
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<212> PRT  
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<220>  
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<220>  
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 <223> Consensus sequence, each Xaa is any amino acid

<400> 20

Xaa Ser Xaa Xaa Xaa Ser Xaa  
 1 5

<210> 21  
 <211> 9  
 <212> PRT  
 <213> Unknown

<220>  
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<220>  
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<400> 21

Gly Ser Ser Lys Ser Lys Pro Lys Asp  
 1 5

<210> 22  
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 <212> PRT  
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<400> 22

Gly Cys Ile Lys Ser Lys Arg Lys Asp  
 1 5

<210> 23  
 <211> 9  
 <212> PRT  
 <213> Unknown

<220>  
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<220>  
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<223> Consensus sequence

<400> 23

Gly Cys Ile Lys Ser Lys Glu Asp Lys  
1 5

<210> 24  
<211> 9  
<212> PRT  
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<220>  
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<400> 24

Gly Cys Val Gln Cys Lys Asp Lys Glu  
1 5

<210> 25  
<211> 9  
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<213> Unknown

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<400> 25

Gly Cys Thr Leu Ser Ala Glu Asp Lys  
1 5

<210> 26  
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<400> 26

Gly Cys Ile Lys Ser Lys Arg Lys Asp  
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<400> 27

Gly Cys Val Gln Cys Lys Asp Lys Glu  
1 5

<210> 28  
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<212> PRT  
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<400> 28

Gly Cys Thr Leu Ser Ala Glu Asp Lys  
1 5

<210> 29  
<211> 4  
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<400> 29

Asn Xaa Ser Thr  
 1

<210> 30  
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<400> 30

His Ser Thr Val  
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 ggggggagct ctgggaggcg gaggtggagg gctgatgcgc cagctgcagg atgaagttga 60  
 agaactggaa caggaaaact ggcattctgca ga 92

<210> 32  
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<223> Synthetic primer .

<220>

<221> misc\_feature

<222> (1)..(96)

<223> Synthetic primer

<400> 32

ccccccctcga gttattaaac ttcggcttcc aggcactgaa cttcacgcag cagacgggca 60

acttcgttct gcagatgccca gttttcctgt tccagt 96

<210> 33

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Coiled-coil sequence

<220>

<221> DOMAIN

<222> (1)..(37)

<223> Coiled coil sequence

<400> 33

Leu Met Arg Gln Leu Gln Asp Glu Val Glu Glu Leu Glu Gln Glu Asn  
1 5 10 15

Trp His Leu Gln Asn Glu Val Ala Arg Leu Leu Arg Glu Val Gln Cys  
20 25 30

Leu Glu Ala Glu Val  
35

<210> 34

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Coiled coil sequence

<220>

<221> DOMAIN

<222> (1)..(37)

<223> Coiled coil sequence

<400> 34

Arg Met Arg Gln Leu Glu Asp Arg Val Glu Glu Leu Arg Glu Gln Asn  
1 5 10 15

Trp His Leu Ala Asn Gln Val Ala Arg Leu Arg Gln Arg Val Cys Glu  
 20 25 30

Leu Lys Ala Arg Val  
 35

<210> 35  
 <211> 80  
 <212> DNA  
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<220>  
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<400> 35  
 gtaccgctag ctcttacaag ggtattgctc agttggagca ggaaatcgcc caattagaac 60  
 aagaaaatgc acaacttgaa 80

<210> 36  
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<220>  
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<220>  
 <221> misc\_feature  
 <222> (1)..(61)  
 <223> Synthetic primer

<400> 36  
 gggcatcgat ttctgtctca agctgagcga tctcttggtc aagttgtgca ttttcttggt 60  
 ctaattgggc gat 73

<210> 37  
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 <213> Unknown

<220>  
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<220>  
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<222> (1)..(31)  
<223> Sequence for cloning

<400> 37

Tyr Lys Gly Ile Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln  
1 5 10 15

Glu Asn Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln Glu  
20 25 30

<210> 38  
<211> 38  
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<220>  
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<223> Coiled coil sequence

<400> 38

Tyr Lys Gly Ile Cys Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln  
1 5 10 15

Arg Asn Ala Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln Arg Ile  
20 25 30

Ala Gln Leu Arg Gln Arg  
35

<210> 39  
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<400> 39

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly  
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr

20

25

30

Asp Val Leu Asp  
35

<210> 40  
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<400> 40

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly  
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr  
20 25 30

Asp Val Leu Asp  
35

<210> 41  
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gggatccata tgccagaccc cgcggcgcac ctg

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<220>  
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ggaattcggg cactgctgtt ggggcaggcc tcc

33

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<400> 44  
ggggggcccga gccccccgcg tac

23

<210> 45  
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<400> 45  
gggggcccaa ccagctctat aac

23

<210> 46  
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<400> 46  
ggggatccgc gagggggcag ggc

23

<210> 47  
<211> 36  
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<220>  
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<400> 47

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly  
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr  
20 25 30

Asp Val Leu Asp  
35

<210> 48  
<211> 6  
<212> PRT  
<213> Unknown

<220>  
<223> Cleavage site

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<223> Xaa is any amino acid

<400> 48

Trp Leu Glu His Asp Xaa  
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<210> 49  
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<223> Cleavage site, each Xaa is any amino acid

<400> 49

Asp Glu Xaa Asp Xaa  
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<210> 50  
<211> 6  
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<220>  
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<400> 50

Leu Val Glu Xaa Asp Xaa  
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<210> 51  
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<212> PRT  
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<220>  
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<400> 51

Ile Glu Gly Arg Xaa  
1 5

<210> 52  
<211> 8  
<212> PRT  
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<220>  
<223> Cleavage site

<220>  
<221> SITE  
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<400> 52

Glu Asn Xaa Tyr Xaa Gln Ser Gly  
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<210> 53  
<211> 5  
<212> PRT  
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<223> Tag peptide

<220>  
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<400> 53

Arg Tyr Ile Arg Ser  
1 5

<210> 54  
<211> 6  
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<400> 54

Asp Thr Tyr Arg Tyr Ile  
1 5

<210> 55  
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<400> 55

Thr Asp Phe Leu Tyr Lys  
1 5

<210> 56  
<211> 9  
<212> PRT  
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<220>  
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<220>  
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<400> 56

Glu Glu Glu Glu Tyr Met Pro Met Glu  
1 5

<210> 57  
<211> 11  
<212> PRT  
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<220>  
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<220>  
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<223> Tag sequence

<400> 57

Lys	Pro	Pro	Thr	Pro	Pro	Pro	Glu	Pro	Glu	Thr
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